

Supplementary file S2

Changes to the LTP classification

Rhodonellum was listed in the LTP s123 classification (Yarza et al., 2008), which is derived from LPSN (Euzéby, 1997), as belonging to *Cytophagaceae*. In the description of the genus *Rhodonellum* (Schmidt et al., 2006) it was placed within the family “*Flexibacteraceae*”. According to a later study (Ying et al., 2006), its most closely related genera are *Algoriphagus*, *Aquiflexum*, *Belliella*, *Chimaereicella*, *Cyclobacterium* and *Hongiella*; among those, *Chimaereicella* and *Hongiella* have been reclassified into *Algoriphagus* (Nedashkovskaya et al., 2007). Accordingly, *Algoriphagus*, *Aquiflexum*, *Belliella*, *Cyclobacterium*, *Echinicola* and *Rhodonellum* have been assigned to *Cyclobacteriaceae* (Nedashkovskaya and Ludwig, 2011; Euzéby, 2012).

An affiliation to a family for *Saccharicrinis* was missing in the LTP s123 classification but provided in the literature (Yang et al., 2014). *Thermonema* was listed in the LTP s123 classification as belonging to *Flammeovirgaceae*. But according to the literature (Nedashkovskaya and Ludwig, 2011a) *Flammeovirgaceae* comprise *Flexithrix*, *Fabibacter*, *Flammeovirga*, *Persicobacter*, *Reichenbachiella* and *Roseivirga*, whereas *Thermonema* is classified as incertae sedis (The editorial board, 2011).

The closely related genera *Aliifodinibius*, *Balneola*, *Fodinibius*, and *Gracilimonas* are listed in LTP/LPSN under the family *Chitinophagaceae*. The family *Chitinophagaceae* originally comprised the genera *Chitinophaga* and *Terrimonas* (Ii, 2010). The new genus *Balneola* was described as belonging to the family *Crenotrichaceae* (Urios et al., 2006). However, the genus *Crenothrix* was later on assigned to *Methylococcales* (Stoecker et al., 2006). Thus, all other *Crenotrichaceae* genera were then considered as *Sphingobacteriales* incertae sedis (Urios et al., 2008). Much like *Balneola*, the genera *Fodinibius* (Wang et al., 2012), *Aliifodinibius* (Wang et al., 2013) and *Gracilimonas* (Choi et al., 2009) were classified as *Sphingobacteriales* incertae sedis (class *Cytophagia*) (Nakagawa, 2011a; Euzéby, 2012). Therefore it remains unclear why these genera have been placed into the family *Chitinophagaceae* by LTP/LPSN.

A couple of species were not included in our comprehensive *Bacteroidetes* 16S rRNA gene tree because in contrast to the LTP/LPSN classification they are not taxonomically classified in *Bacteroidetes* any more. *Anaerorhabdus* with its sole species *A. furcosa* is listed as belonging to *Bacteroidaceae*, whereas a recent monography (Rosenberg et al., 2013) assigns it to *Erysipelotrichaceae* (*Firmicutes*) because if its phylogenetic placement in 16S rRNA gene trees. *Acetomicrombium faecale* has been reclassified into the genus *Caldicoprobacter* (*Firmicutes*) as *C. faecalis* (Ben

Hania et al., 2015). The remaining (and type) species in *Acetomicrobium*, *A. flavidum*, is placed within *Synergistetes* in 16S rRNA gene trees (Yarza et al., 2008), thus *Acetomicrobium* should not be classified as within *Bacteroidaceae* as in the LTP/LPSN classification but outside the *Bacteroidetes*. *Bacteroides cellulosolvens* should not separately be listed in the LTP/LPSN classification because it is a homotypic synonym of *Pseudobacteroides cellulosolvens* (*Firmicutes*) (Horino et al., 2014). Similarly, *Flexibacter aurantiacus* is a homotypic synonym of *Flavobacterium johnsoniae* (Bernardet et al., 1996).

Flavobacterium oceanosedimentum (*Flavobacteriaceae*) has been reclassified as *Curtobacterium oceanosedimentum* (*Actinobacteria*) (Kim et al., 2009) but this name has not been regarded as validly published. For *Bacteroides coagulans*, *B. galacturonicus* and *B. pectinophilus* new combinations have not yet been proposed but phylogenetically they are not only placed outside *Bacteroides* but even outside *Bacteroidetes* (Yarza et al., 2008). For this reason, they were not included in our comprehensive *Bacteroidetes* 16S rRNA gene tree either.

Prolixibacteraceae comprise the genera *Prolixibacter*, *Sunxiuqinia* and *Mangrovibacterium* (Huang et al., 2014). *Prolixibacteraceae* are an earlier heterotypic synonym of *Draconibacteriaceae* (Du et al., 2014) and thus comprise additionally the genera *Draconibacterium*, *Mariniphaga* and *Meniscus* (Iino et al., 2014). The genus *Marinifilum* belongs to the family *Marinilaceae* (order *Bacteroidales*) (Iino et al., 2014).

A couple of sequences of interest were missing from the LTP s123 release, including the type species of the genus *Thermonema*, *T. lapsum* (HE582775) (Hudson et al., 1989); *Saprospira grandis* (M58795); and *Epilithonimonas psychrotolerans* (DQ173014). Moreover, AB078062 is incorrect a sequence of the type strain of *Flexibacter roseolus*; AB078063 should be chosen instead (Nakagawa et al., 2002).

Ignavibacterium (family *Ignavibacteriaceae*, order *Ignavibacteriales*, class *Ignavibacteria*) was first placed in the phylum *Chlorobi* (Iino et al., 2010). However, with the description of the new genus *Melioribacter* within the new family *Melioribacteraceae*, the class *Ignavibacteria* was placed into the new phylum *Ignavibacteriae* (Oren and Garrity, 2016; Podosokorskaya et al., 2013).

The new families *Catalimonadaceae* (comprising the genera *Catalinimonas*, ‘*Porifericola*’ and ‘*Tunicatimonas*’) and *Mooreiaceae* (comprising the genus *Mooreia*) were recently suggested (Choi et al., 2013). This resulted into a split of the family *Flammeovirgaceae* into the core *Flammeovirgaceae* (comprising the genera *Flammeovirga*, *Perexilibacter*, *Limibacter*, *Sediminitomix*, *Rapidithrix*, *Flexithrix*, *Persicobacter* and *Aureibacter*) and a taxonomically unresolved branch (comprising the

genera *Cesiribacter*, *Marivirga*, *Roseivirga*, *Fabibacter*, *Reichenbachia*, *Fulvivirga* and *Marinoscillum*) (Choi et al., 2013).

A variety of changes to the classification were made in a recent study (Munoz et al., 2016) using 16S rRNA gene and MLSA phylogenies (for which no branch support was presented). *Butyricimonas* and *Odoribacter* were placed in a family of their own, *Odoribacteraceae*, whereas *Crocinitomix* and *Fluviicola* were placed in the new family *Crocinitomicaceae* together with *Brumimicrobium*, *Lishizhenia*, *Salinirepens* and *Wandonia*. *Adhaeribacter*, *Hymenobacter*, *Nibribacter*, *Pontibacter* and *Rufibacter* were placed in the new family *Hymenobacteraceae* but *Aureibacter*, *Fulvitalea* and *Persicobacter* in *Persicobacteraceae*. For *Thermonema* the new family *Thermonemataceae* was introduced, and for the *Chitinophagaceae* and *Saprospiraceae* the new order *Chitinophagales* in the new class *Chitinophagia*. The genera *Persicobacter*, *Aureibacter* and *Fulvitalea* were moved into the new family *Persicobacteraceae*. Finally, the new phylum *Rhodothermaeota* was established, comprising the classes *Balneolia* and *Rhodothermia* with the sole orders *Balneolales* and *Rhodothermales*, respectively. *Balneolaceae* were introduced to harbor *Aliifodinibius*, *Balneola*, *Fodinibius* and *Gracilimonas*, *Salinibacteraceae* to comprise *Salinibacter*, *Salisaeta* and *Salinivenus* (a genus newly introduced for *Salinibacter iranicus* and *S. luteus*), and *Rubricoccaceae* to contain *Rubricoccus* and *Rubrivirga*, thus restricting *Rhodothermaceae* to *Rhodothermus*.

Other taxonomic notes

The genus *Flexithrix* is listed in LPSN in the family *Flammeovirgaceae*. This is consistent with Bergey's Manual of Systematic Bacteriology (Nedashkovskaya and Ludwig, 2011a). The family *Flammeovirgaceae* (Nedashkovskaya and Ludwig, 2011a) comprises the genera *Flexithrix* as well as *Fabibacter*, *Flammeovirga*, *Persicobacter*, *Reichenbachiella* and *Roseivirga* (Nedashkovskaya and Ludwig, 2011a). *Flexithrix dorotheae* Lewin 1970 (Approved Lists 1980) is an earlier heterotypic synonym of *Flexibacter aggregans* (Lewin 1969) Leadbetter 1974 (Approved Lists 1980) (Hosoya and Yokota, 2007). *Flexithrix dorotheae* is the type species of the genus and the only type train in the genus. See notes on "Flexibacter" below.

The genus *Marivirga* is listed in LPSN in the family *Flammeovirgaceae*. The family *Flammeovirgaceae* comprises the genera *Flexithrix* as well as *Fabibacter*, *Flammeovirga*, *Persicobacter*, *Reichenbachiella* and *Roseivirga* (Nedashkovskaya and Ludwig, 2011a). Based on the results of Nakagawa et al. (Nakagawa et al., 2002) and a polyphasic approach by Nedashkovskaya et al. (Nedashkovskaya et al., 2010), the genus *Marivirga* was proposed comprising *Marivirga tractuosa* (*Flexibacter tractuosus*

(Lewin 1969) Leadbetter 1974) and *Marivirga sericea* (“*Microscilla sericea*” Lewin 1969) (Nedashkovskaya and Ludwig, 2011a).

Owenweeksia hongkongensis (Lau et al., 2005; Zhou et al., 2013) is listed in LPSN under the family *Cryomorphaceae*. This is consistent with Bergey’s Manual of Systematic Bacteriology (Nedashkovskaya and Ludwig, 2011a). The family *Cryomorphaceae* (Bowman, 2011) comprises the genera *Brumimicrobium*, *Crocinitomix*, *Cryomorpha*, *Fluviicola*, *Lishizhenia*, *Owenweeksia* (Bowman, 2011; Lee et al., 2010), as well as the genera *Phaeocystidibacter* (Zhou et al., 2013), *Salinirepens* (Muramatsu et al., 2012), *Luteibaculum* (Shahina et al., 2013) and *Wandonia* (Lee et al., 2010; Muramatsu et al., 2012).

The genus *Flexibacter* is listed in LPSN in the family *Cytophagaceae*. This is consistent with Bergey’s Manual of Systematic Bacteriology (Nedashkovskaya and Ludwig, 2011a). The family *Cytophagaceae* comprises the genera *Flexibacter* as well as *Adhaeribacter*, *Arcicella*, *Cytophaga*, *Dyadobacter*, *Effluvibacter*, *Emiticia*, *Flectobacillus*, *Hymenobacter*, *Larkinella*, *Leadbetterella*, *Meniscus*, *Microscilla*, *Pontibacter*, *Runella*, *Spirosoma* and *Sporocytophaga* (Nakagawa, 2011b).

Recently the family *Rhodothermaceae* (Ludwig W, Euzeby J, 2011; Euzéby, 2012) was validly named (incertae sedis, class *Cytophagia*), comprising the genera *Rhodothermus* and *Salinibacter* (Oren and Garrity, 2015), as well as the genera *Rubricoccus* (Park et al., 2011), *Rubrivirga* (Park et al., 2013) and *Salisaeta* (Vaisman and Oren, 2009).

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